AMENDMENTS TO THE CLAIMS:

Claims 1-54 are pending in the subject application. It is proposed that each of claims 1, 29, 34, 46, and 51-54 be amended as set forth herein and claims 4-8 be canceled. All claims currently pending and under consideration in the referenced application are shown below. Upon entry of the proposed amendments, this listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method in a computing environment for documenting mutations, the method comprising:

receiving mutation information;

disassembling the mutation information into discrete elements including a patient identification value, a mutation type, a reference sequence identification value, a starting point value within a reference sequence, and an ending point within the reference sequence;

storing said discrete elements such that the mutation may be presented using both user-preferred and published standards; and

displaying ~~presenting~~ the mutation using the user-preferred standard, the published standard, or a combination thereof.

2. (Previously Presented) The method of claim 1, wherein the mutation information is for one of a substitution, inversion, insertion, deletion, translocation, complex rearrangement and combinations thereof.

3. (Withdrawn) The method of claim 1, wherein the discrete elements include a mutation identification value.

4. (Canceled)

5. (Canceled)

6. (Canceled)

7. (Canceled)

8. (Canceled)

9. (Withdrawn) The method of claim 1, wherein the discrete elements include the length of an insertion.

10. (Withdrawn) The method of claim 1, wherein the discrete elements include the native value of sequenced genetic information.

11. (Original) The method of claim 1, wherein the discrete elements include an observed value of the mutation.

12. (Original) The method of claim 10, wherein the native value of sequenced genetic information is one or more nucleotides or amino acids.

13. (Original) The method of claim 11, wherein the observed value of sequenced genetic information is one or more nucleotides or amino acids.

14. (Original) The method of claim 1, wherein the user-preferred standards are user defined.

15. (Original) The method of claim 1, wherein the published standards are the recommended standards published the Human Genome Association.

16. (Withdrawn) The method of claim 1, wherein the published standards are the standards adopted by the genetics community.

17. (Original) The method of claim 1, further comprising:

providing a list of known mutations for particular sequenced genetic information.

18. (Original) The method of claim 17, wherein the sequenced genetic information is one of a gene, a protein, sequenced DNA other than a gene and sequenced RNA.

19. (Original) The method of claim 18, further comprising:

receiving a selection of a mutation from the list of known mutations.

20. (Original) The method of claim 17, further comprising:

receiving a request for the reference sequence for the sequenced genetic information.

21. (Original) The method of claim 20, further comprising:

providing the reference sequence for the sequenced genetic information.

22. (Original) The method of claim 21, further comprising:

providing data entry fields for the entry of mutation information.

23. (Original) The method of claim 22, wherein the data entry fields include one or more of the position of the mutation and the value of the mutation.

24. (Original) The method of claim 23, further comprising:

receiving mutation type.

25. (Previously Presented) The method of claim 24, further comprising:

receiving an observed mutation value.

26. (Previously Presented) The method of claim 1, wherein the mutation information is for one of humans, animals, vertebrates, invertebrates, plants, viruses, bacteria, fungi, prokaryotes, eukaryotes, and protista.

27. (Original) The method of claim 26, wherein the mutation information is for a particular patient.

28. (Original) The method of claim 27, further comprising:

identifying the patient in connection with the mutation information and the discrete values.

29. (Currently Amended) A method in a computing environment for presenting mutations, the method comprising:

obtaining ~~the~~ discrete elements for mutation information, wherein the discrete elements include a patient identification value, a reference sequence identification value, a starting point value within a reference sequence, and an ending point within the reference sequence;

obtaining at least one standard for presenting the mutation information;

assembling the mutation information utilizing the discrete elements and the at least one standard of presentation; and

displaying ~~presenting~~ the mutation using the at least one standard of presentation.

30. (Previously Presented) The method of claim 29, wherein the at least one standard of presentation is one or more of a user-preferred standard, a published standard, or a combination thereof.

31. (Original) The method of claim 30, wherein the user-preferred standard is user defined.

32. (Original) The method of claim 30, wherein the published standard is published by the Human Genome Association.

33. (Withdrawn) The method of claim 30, wherein the published standards are the standards adopted by the genetics community.

34. (Currently Amended) A computer system for documenting mutations, the system comprising:

a receiving module for receiving mutation information;

a disassembling module for disassembling the mutation information into discrete elements, wherein the discrete elements include a patient identification value, a reference sequence identification value, a starting point value within a reference sequence, and an ending point within the reference sequence; ~~and~~

a storage module stores said discrete elements such that the mutation may be presented using both user-preferred and published standards[[.]] ; and

a displaying module for displaying the mutation using the user-preferred standard, the published standard, or a combination thereof.

35. (Original) The system of claim 34, wherein the mutation information is for one of a substitution, inversion, insertion, deletion, translocation, complex rearrangement and combinations thereof.

36. (Original) The system of claim 34, wherein the discrete elements include one or more of a mutation identification value, patient identification value, mutation type, reference sequence identification value, starting point value within the reference sequence, ending point within the reference sequence, length of an insertion, native value of sequenced genetic information, observed value of the mutation.

37. (Original) The system of claim 34, wherein the user-preferred standards are user defined.

38. (Original) The system of claim 34, wherein the published standards are the recommended standards published the Human Genome Association.

39. (Withdrawn) The system of claim 34, wherein the published standards are the standards adopted by the genetics community.

40. (Original) The system of claim 34, further comprising:

a providing module for providing a list of known mutations for particular sequenced genetic information.

41. (Original) The system of claim 40, wherein the sequenced genetic information is a gene.

42. (Original) The system of claim 40, further comprising:

a second receiving module for receiving a selection of a mutation from the list of known mutations.

43. (Original) The system of claim 40, further comprising:

a third receiving module receiving a request for the reference sequence for the sequenced genetic information.

44. (Original) The system of claim 43, further comprising:

a second providing component for providing the reference sequence for the sequenced genetic information.

45. (Original) The system of claim 44, further comprising:

a third providing component for providing data entry fields for the entry of mutation information.

46. (Currently Amended) A computer system for presenting mutations, the method comprising:

an obtaining component for obtaining ~~the~~ discrete elements for mutation information, wherein the discrete elements include a patient identification value, a reference sequence identification value, a starting point value within a reference sequence, and an ending point within the reference sequence;

a second obtaining component for obtaining a standard for presenting the mutation information; ~~and~~

an assembling component for assembling the mutation information utilizing the discrete elements and the standard of presentation[[.]] ; and

a displaying component for displaying the mutation in accordance with the standard of presentation.

47. (Original) The system of claim 46, wherein the standard is one of a user-preferred standard and a published standard.

48. (Original) The system of claim 47, wherein the user-preferred standard is user defined.

49. (Original) The system of claim 47, wherein the published standard is published by the Human Genome Association.

50. (Withdrawn) The system of claim 47, wherein the published standards are the standards adopted by the genetics community.

51. (Currently Amended) A computer-readable medium having computer-executable instructions for performing a method, the method comprising:

receiving mutation information;

disassembling the mutation information into discrete elements including a patient identification value, a reference sequence identification value, a starting point value within a reference sequence, and an ending point within the reference sequence;

storing said discrete elements such that the mutation may be presented using both user-preferred and published standards; and

displaying ~~presenting~~ the mutation using the user-preferred standard, the published standard, or a combination thereof.

52. (Currently Amended) A computer-readable medium having computer-executable instructions for performing a method, the method comprising:

obtaining discrete elements for a mutation, wherein the discrete elements include a patient identification value, a reference sequence identification value, a starting point value within a reference sequence, and an ending point within the reference sequence;

obtaining at least one standard for presenting the mutation information;

assembling the mutation information utilizing the discrete elements and the at least one standard of presentation; and

displaying ~~presenting~~ the mutation using the at least one standard of presentation.

53. (Currently Amended) A computer system for documenting mutations, the method comprising:

means for receiving mutation information;

means for disassembling the mutation information into discrete elements, wherein the discrete elements include a patient identification value, a reference sequence identification value, a starting point value within a reference sequence, and an ending point within the reference sequence; ~~and~~

means for storing said discrete elements such that the mutation may be presented using both user-preferred and published standards[[.]]; and

means for displaying the mutation using the user-preferred standard, the published standard, or a combination thereof.

54. (Currently Amended) A computer system for presenting mutations, the method comprising:

means for obtaining ~~the~~ discrete elements for mutation information, wherein the discrete elements include a patient identification value, a reference sequence identification value, a starting point value within a reference sequence, and an ending point within the reference sequence;

means for obtaining a standard for presenting the mutation information; ~~and~~

means for assembling the mutation information utilizing the discrete elements and the standard of presentation[[.]]; and

means for displaying the mutation using the user-preferred standard, the published standard, or a combination thereof.

55-64 (Canceled).